```
GGA TCC GGC TCC GGA ACG GAT TAC ACT CTG 300
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
                70                  75

ACC ATC AGC AGT CTG CAA CCT GAG GAC TTC 330
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                80                  85

GCT ACG TAT TAC TGT CAG AAC GTT TTA AAT 360
Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn
                90                  95

ACT CCG TTG ACT TTC GGA CAG GGT ACC AAG 390
Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys
               100                 105

GTG GAA ATA AAA CGA ACT GTG GCT GCA CCA 420
Val Glu Ile Lys Arg Thr Val Ala Ala Pro
               110                 115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
               120                 125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val
               130                 135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
               140                 145

GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala
               150                 155
```

```
CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
                160                 165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
                170                 175

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                180                 185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
                190                 195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690
Cys Glu Val Thr His Gln Gly Leu Ser Ser
                200                 205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                210                 215

TGT TAG                             726
Cys
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: SG1.1 VL +KLV56B (Humanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30
Met Gly Ile Gln Gly Gly Ser Val Leu Phe
-25              -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60
Gly Leu Leu Leu Val Leu Ala Val Phe Cys
-15              -10

CAT TCA GGT CAT AGC CTG CAG GAT ATC CAG 90
His Ser Gly His Ser Leu Gln Asp Ile Gln
-5                1                5

ATG ACC CAG TCC CCG TCC TCC CTG TCC GCC 120
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
                 10                  15

TCT GTG GGC GAT AGG GTC ACC ATC ACC TGC 150
Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                 20                  25

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu
                 30                  35

AAC TGG TAT CAA CGT AAA CCT GGG AAA GCT 210
Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala
                 40                  45

CCG AAG CTT CTG ATT TAC GGT GCG ACG AAC 240
Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn
                 50                  55

CTG GCA GAT GGA GTC CCT TCT CGC TTC TCT 270
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser
                 60                  65
```

```
GGA TCC GGC TCC GGA ACG GAT TTC ACT CTG 300
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                70                  75

ACC ATC AGC AGT CTG CAG CCT GAA GAC TTC 330
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                80                  85

GCT ACG TAT TAC TGT CAG AAC GTT TTA AAT 360
Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn
                90                  95

ACT CCG TTG ACT TTC GGA CAG GGT ACC AAG 390
Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys
               100                 105

GTG GAA ATA AAA CGA ACT GTG GCT GCA CCA 420
Val Glu Ile Lys Arg Thr Val Ala Ala Pro
               110                 115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
               120                 125

CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val
               130                 135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
               140                 145

GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala
               150                 155
```

```
CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
                160                 165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
                170                 175

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                180                 185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
                190                 195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690
Cys Glu Val Thr His Gln Gly Leu Ser Ser
                200                 205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                210                 215

TGT TAG                                 726
Cys
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 VL + 012 (Humanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
ATG GAC ATG AGG GTC CCC GCT CAG CTC CTG 30
Met Asp Met Arg Val Pro Ala Gln Leu Leu
        -20                 -15

GGG CTC CTG CTA CTC TGG CTC CGA GGT GCC 60
Gly Leu Leu Leu Leu Trp Leu Arg Gly Ala
    -10                 -5

AGA TGT GAT ATC CAG ATG ACC CAG TCC CCG 90
Arg Cys Asp Ile Gln Met Thr Gln Ser Pro
 1               5

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 120
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 10                  15

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 150
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
 20                  25

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 180
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln
 30                  35

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 210
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 40                  45

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 240
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val
 50                  55

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 270
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 60                  65
```

```
ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 300
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
     70                  75

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 330
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
     80                  85

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 360
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
     90                  95

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGA 390
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
    100                 105

ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC 420
Thr Val Ala Ala Pro Ser Val Phe Ile Phe
    110                 115

CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA 450
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
    120                 125

ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC 480
Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135

TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG 510
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
    140                 145

AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC 540
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
    150                 155
```

```
TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC 570
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
    160                 165

AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC 600
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
    170                 175

CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 630
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
    180                 185

CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT 660
His Lys Val Tyr Ala Cys Glu Val Thr His
    190                 195

CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC 690
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
    200                 205

TTC AAC AGG GGA GAG TGT TAG             711
Phe Asn Arg Gly Glu Cys
    210
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 VH + IGHRLD (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30
Met Lys Trp Ser Trp Val Ile Leu Phe Leu
               -15                 -10

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60
Leu Ser Val Thr Ala Gly Val His Ser Gln
            -5                   1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90
Val Gln Leu Val Gln Ser Gly Ala Glu Val
          5                   10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120
Lys Lys Pro Gly Ala Ser Val Lys Val Ser
          15                  20

TGT AAA GCT AGC GGC TAT ATT TTT TCT AAT 150
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn
          25                  30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro
          35                  40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile
          45                  50

TTA CCG GGC TCT GGT AGC ACC GAA TAT GCC 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala
          55                  60

CAA AAA TTC CAG GGC CGT GTT ACT ATG ACT 270
Gln Lys Phe Gln Gly Arg Val Thr Met Thr
          65                  70
```

```
CGT GAC ACT TCG ACT AGT ACA GTA TAC ATG 300
Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
            75                  80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            85                  90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
            95                  100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
            105                 110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            115                 120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
            125                 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
            135                 140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
            145                 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
            155                 160
```

```
TCG TGG AAC TCA GGC GCC CTG ACC AAC GGC 570
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            165                 170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600
Val His Thr Phe Pro Ala Val Leu Gln Ser
            175                 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            185                 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
            195                 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690
Thr Tyr Ile Cys Asn Val Asn His Lys Pro
            205                 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720
Ser Asn Thr Lys Val Asp Lys Lys Val Glu
            215                 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750
Pro Lys Ser Cys Asp Lys Thr His Thr
            225                 230
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 scFv.D012
(Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30
Met Ala Asp Ile Gln Met Thr Gln Ser Pro
 1               5                  10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
                15                  20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
            25                  30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln
        35                  40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    45                  50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val
55                  60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65                  70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
            75                  80
```

```
CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
                85                  90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
                95                  100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
                105                 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
                115                 120

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
                125                 130

GTG CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
                135                 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
                145                 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
                155                 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
                165                 170
```

```
CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Pro Gly
                175                 180

TCT GGT AGC ACC GAA TAT GCC CAA AAA TTC 570
Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe
                185                 190

CAG GGC CGT GTT ACT ATG ACG CGT GAC ACT 600
Gln Gly Arg Val Thr Met Thr Arg Asp Thr
                195                 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                205                 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
                215                 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
                225                 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
                235                 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA      747
Gly Thr Leu Val Thr Val Ser Ser
                245
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5248 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: pET Trc S05/NI prokaryotic expression vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG 50

TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT 100

CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCCCG 150

TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT AGTGCTTTAC 200

GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG 250

CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT 300

CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCCTATCT 350

CGGTCTATTC TTTTGATTTA TAAGGGATTT TGCCGATTTC GGCCTATTGG 400

TTAAAAAATG AGCTGATTTA ACAAAAATTT AACGCGAATT TTAACAAAAT 450

ATTAACGTTT ACAATTTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA 500

CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG 550

AGACAATAAC CCTGATAAAT GCTTCAATAA TATTGAAAAA GGAAGAGTAT 600

GAGTATTCAA CATTTCCGTG TCGCCCTTAT TCCCTTTTTT GCGGCATTTT 650

GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT AAAAGATGCT 700

GAAGATCAGT TGGGTGCACG AGTGGGTTAC ATCGAACTGG ATCTCAACAG 750

CGGTAAGATC CTTGAGAGTT TTCGCCCCGA AGAACGTTTT CCAATGATGA 800

GCACTTTTAA AGTTCTGCTA TGTGGCGCGG TATTATCCCG TATTGACGCC 850

GGGCAAGAGC AACTCGGTCG CCGCATACAC TATTCTCAGA ATGACTTGGT 900

TGAGTACTCA CCAGTCACAG AAAAGCATCT TACGGATGGC ATGACAGTAA 950

GAGAATTATG CAGTGCTGCC ATAACCATGA GTGATAACAC TGCGGCCAAC 1000

TTACTTCTGA CAACGATCGG AGGACCGAAG GAGCTAACCG CTTTTTTGCA 1050

CAACATGGGG GATCATGTAA CTCGCCTTGA TCGTTGGGAA CCGGAGCTGA 1100

ATGAAGCCAT ACCAAACGAC GAGCGTGACA CCACGATGCC TGCAGCAATG 1150

GCAACAACGT TGCGCAAACT ATTAACTGGC GAACTACTTA CTCTAGCTTC 1200

CCGGCAACAA TTAATAGACT GGATGGAGGC GGATAAAGTT GCAGGACCAC 1250

TTCTGCGCTC GGCCCTTCCG GCTGGCTGGT TTATTGCTGA TAAATCTGGA 1300

GCCGGTGAGC GTGGGTCTCG CGGTATCATT GCAGCACTGG GGCCAGATGG 1350

TAAGCCCTCC CGTATCGTAG TTATCTACAC GACGGGGAGT CAGGCAACTA 1400

TGGATGAACG AAATAGACAG ATCGCTGAGA TAGGTGCCTC ACTGATTAAG 1450

CATTGGTAAC TGTCAGACCA AGTTTACTCA TATATACTTT AGATTGATTT 1500

AAAACTTCAT TTTTAATTTA AAAGGATCTA GGTGAAGATC CTTTTTGATA 1550

ATCTCATGAC CAAAATCCCT TAACGTGAGT TTTCGTTCCA CTGAGCGTCA 1600

GACCCCGTAG AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTCTGCG 1650

CGTAATCTGC TGCTTGCAAA CAAAAAAACC ACCGCTACCA GCGGTGGTTT 1700

GTTTGCCGGA TCAAGAGCTA CCAACTCTTT TTCCGAAGGT AACTGGCTTC 1750

AGCAGAGCGC AGATACCAAA TACTGTCCTT CTAGTGTAGC CGTAGTTAGG 1800

CCACCACTTC AAGAACTCTG TAGCACCGCC TACATACCTC GCTCTGCTAA 1850

TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG 1900

TTGGACTCAA GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC 1950

GGGGGGTTCG TGCACACAGC CCAGCTTGGA GCGAACGACC TACACCGAAC 2000

TGAGATACCT ACAGCGTGAG CTATGAGAAA GCGCCACGCT TCCCGAAGGG 2050

AGAAAGGCGG ACAGGTATCC GGTAAGCGGC AGGGTCGGAA CAGGAGAGCG 2100

CACGAGGGAG CTTCCAGGGG GAAACGCCTG GTATCTTTAT AGTCCTGTCG 2150

GGTTTCGCCA CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG 2200

GGGCGGAGCC TATGGAAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT 2250

GGCCTTTTGC TGGCCTTTTG CTCACATGTT CTTTCCTGCG TTATCCCCTG 2300

ATTCTGTGGA TAACCGTATT ACCGCCTTTG AGTGAGCTGA TACCGCTCGC 2350

CGCAGCCGAA CGACCGAGCG CAGCGAGTCA GTGAGCGAGG AAGCGGAAGA 2400

GCGCCTGATG CGGTATTTTC TCCTTACGCA TCTGTGCGGT ATTTCACACC 2450

GCATATATGG TGCACTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA 2500

GCCAGTATAC ACTCCGCTAT CGCTACGTGA CTGGGTCATG GCTGCGCCCC 2550

GACACCCGCC AACACCCGCT GACGCGCCCT GACGGGCTTG TCTGCTCCCG 2600

GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA 2650

GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGGCAGCTG CGGTAAAGCT 2700

CATCAGCGTG GTCGTGAAGC GATTCACAGA TGTCTGCCTG TTCATCCGCG 2750

TCCAGCTCGT TGAGTTTCTC CAGAAGCGTT AATGTCTGGC TTCTGATAAA 2800

GCGGGCCATG TTAAGGGCGG TTTTTTCCTG TTTGGTCACT GATGCCTCCG 2850

TGTAAGGGGG ATTTCTGTTC ATGGGGGTAA TGATACCGAT GAAACGAGAG 2900

AGGATGCTCA CGATACGGGT TACTGATGAT GAACATGCCC GGTTACTGGA 2950

ACGTTGTGAG GGTAAACAAC TGGCGGTATG GATGCGGCGG GACCAGAGAA 3000

AAATCACTCA GGGTCAATGC CAGCGCTTCG TTAATACAGA TGTAGGTGTT 3050

CCACAGGGTA GCCAGCAGCA TCCTGCGATG CAGATCCGGA ACATAATGGT 3100

GCAGGGCGCT GACTTCCGCG TTTCCAGACT TTACGAAACA CGGAAACCGA 3150

AGACCATTCA TGTTGTTGCT CAGGTCGCAG ACGTTTTGCA GCAGCAGTCG 3200

CTTCACGTTC GCTCGCGTAT CGGTGATTCA TTCTGCTAAC CAGTAAGGCA 3250

ACCCCGCCAG CCTAGCCGGG TCCTCAACGA CAGGAGCACG ATCATCGCGA 3300

CCCGTGGGGC CGCCATGCCG GCGATAATGG CCTGCTTCTC GCCGAAACGT 3350

TTGGTGGCGG GACCAGTGAC GAAGGCTTGA GCGAGGGCGT GCAAGATTCC 3400

GAATACCGCA AGCGACAGGC CGATCATCGT CGCGCTCCAG CGAAAGCGGT 3450

CCTCGCCGAA AATGACCCAG AGCGCTGCCG GCACCTGTCC TACGAGTTGC 3500

ATGATAAAGA AGACAGTCAT AAGTGCGGCG ACGATAGTCA TGCCCCGCGC 3550

CCACCGGAAG GAGCTGACTG GGTTGAAGGC TCTCAAGGGC ATCGGTCGAG 3600

ATCCCGGTGC CTAATGAGTG AGCTAACTTA CATTAATTGC GTTGCGCTCA 3650

CTGCCCGCTT TCCAGTCGGG AAACCTGTCG TGCCAGCTGC ATTAATGAAT 3700

CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC CAGGGTGGTT 3750

TTTCTTTTCA CCAGTGAGAC GGGCAACAGC TGATTGCCCT TCACCGCCTG 3800

GCCCTGAGAG AGTTGCAGCA AGCGGTCCAC GCTGGTTTGC CCCAGCAGGC 3850

GAAAATCCTG TTTGATGGTG GTTAACGGCG GGATATAACA TGAGCTGTCT 3900

TCGGTATCGT CGTATCCCAC TACCGAGATA TCCGCACCAA CGCGCAGCCC 3950

GGACTCGGTA ATGGCGCGCA TTGCGCCCAG CGCCATCTGA TCGTTGGCAA 4000

CCAGCATCGC AGTGGGAACG ATGCCCTCAT TCAGCATTTG CATGGTTTGT 4050

TGAAAACCGG ACATGGCACT CCAGTCGCCT TCCCGTTCCG CTATCGGCTG 4100

AATTTGATTG CGAGTGAGAT ATTTATGCCA GCCAGCCAGA CGCAGACGCG 4150

CCGAGACAGA ACTTAATGGG CCCGCTAACA GCGCGATTTG CTGGTGACCC 4200

AATGCGACCA GATGCTCCAC GCCCAGTCGC GTACCGTCTT CATGGGAGAA 4250

AATAATACTG TTGATGGGTG TCTGGTCAGA GACATCAAGA AATAACGCCG 4300

GAACATTAGT GCAGGCAGCT TCCACAGCAA TGGCATCCTG GTCATCCAGC 4350

GGATAGTTAA TGATCAGCCC ACTGACGCGT TGCGCGAGAA GATTGTGCAC 4400

CGCCGCTTTA CAGGCTTCGA CGCCGCTTCG TTCTACCATC GACACCACCA 4450

CGCTGGCACC CAGTTGATCG GCGCGAGATT TAATCGCCGC GACAATTTGC 4500

GACGGCGCGT GCAGGGCCAG ACTGGAGGTG GCAACGCCAA TCAGCAACGA 4550

CTGTTTGCCC GCCAGTTGTT GTGCCACGCG GTTGGGAATG TAATTCAGCT 4600

CCGCCATCGC CGCTTCCACT TTTTCCCGCG TTTTCGCAGA AACGTGGCTG 4650

GCCTGGTTCA CCACGCGGGA AACGGTCTGA TAAGAGACAC CGGCATACTC 4700

TGCGACATCG TATAACGTTA CTGGTTTCAC ATTCACCACC CTGAATTGAC 4750

TCTCTTCCGG GCGCTATCAT GCCATACCGC GAAAGGTTTT GCGCCATTCG 4800

ATGGTGTCCG GGATCTCGAC GCTCTCCCTT ATGCGACTCC TGCATTAGGA 4850

AGCAGCCCAG TAGTAGGTTG AGGCCGTTGA GCACCGCCGC CGCAAGGAAT 4900

GGTGCATGCG GTACCAGCTG TTGACAATTA ATCATCCGGC TCGTATAATA 4950

GTACTGTGTG GAATTGTGAG CGCTCACAAT TCCACACATC TAGAAATAAT 5000

TTTGTTTAAC TTTAAGAAGG AGATATACCA TGGAGATCTG GATCCATCGA 5050

TGAATTCGAG CTCCGTCGAC AAGCTTGCGG CCGCACTCGA GCACCACCAC 5100

CACCACCACT GAGATCCGGC TGCTAACAAA GCCCGAAAGG AAGCTGAGTT 5150

GGCTGCTGCC ACCGCTGAGC AATAACTAGC ATAACCCCTT GGGGCCTCTA 5200

AACGGGTCTT GAGGGGTTTT TTGCTGAAAG GAGGAACTAT ATCCGGAT 5248

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: N19/8 scFv (His Tagged)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ATG GCC AAT ATT GTG CTG ACC CAA TCT CCA 30
Met Ala Asn Ile Val Leu Thr Gln Ser Pro
 1               5                  10

GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG 60
Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
                15                  20

GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT 120
Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
                25                  30

GTT GAT AGT TAT GAC AAT AGT TTT ATG CAC 150
Val Asp Ser Tyr Asp Asn Ser Phe Met His
                35                  40

TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC 180
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
                45                  50

AAA CTC CTC ATC TTT CTT GCA TCC AAC CTA 210
Lys Leu Leu Ile Phe Leu Ala Ser Asn Leu
                55                  60

GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC 240
Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
                65                  70

AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC 270
Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr
                75                  80

ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA 300
Ile Asp Pro Val Glu Ala Asp Asp Ala Ala
                85                  90
```

```
ACC TAT TAC TGT CAG CAA AAT AAT GAG GTT 330
Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Val
                95                  100

CCG AAC ACG TTC GGA GGG GGG ACC AAG CTG 360
Pro Asn Thr Phe Gly Gly Gly Thr Lys Leu
            105                 110

GAA ATA AAA CGG ACC GGA GGT GGC GGG TCG 390
Glu Ile Lys Arg Thr Gly Gly Gly Gly Ser
        115                 120

GGT GGC GGG GGA TCG GGT GGC GGA GGG TCG 420
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            125                 130

GAC GTC AAG CTC GTG GAG TCT GGG GGA GAC 450
Asp Val Lys Leu Val Glu Ser Gly Gly Asp
            135                 140

TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC 480
Leu Val Lys Leu Gly Gly Ser Leu Lys Leu
            145                 150

TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT 510
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            155                 160

AGC TAT TAT ATG TCT TGG GTT CGC CAG ATT 540
Ser Tyr Tyr Met Ser Trp Val Arg Gln Ile
            165                 170

TCA GAG AAG AGG CTG GAG TTG GTC GCA GCC 570
Ser Glu Lys Arg Leu Glu Leu Val Ala Ala
            175                 180
```

```
ATT AAT AGT AAT GGT GAT AGC ACC TAC TAT 600
Ile Asn Ser Asn Gly Asp Ser Thr Tyr Tyr
                185                 190

CCA GAC ACT GTG AAG GGC CGA TTC ACC ATC 630
Pro Asp Thr Val Lys Gly Arg Phe Thr Ile
                195                 200

TCC AGA GAC AAT GCC AAG AGC ACC CTG GAT 660
Ser Arg Asp Asn Ala Lys Ser Thr Leu Asp
                205                 210

CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC 690
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
                215                 220

ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 720
Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr
                225                 230

TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 750
Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp
                235                 240

GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 780
Val Trp Gly Thr Gly Thr Thr Val Thr Val
                245                 250

TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 810
Ser Ser Leu Glu His His His His His His
                255                 260

TGA                                     813
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WO 95/29697 PCT/US95/05688

2189015

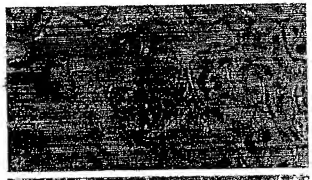

FIG.1A

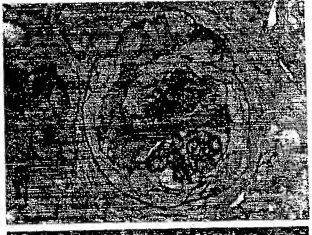

FIG.1B

FIG.1C

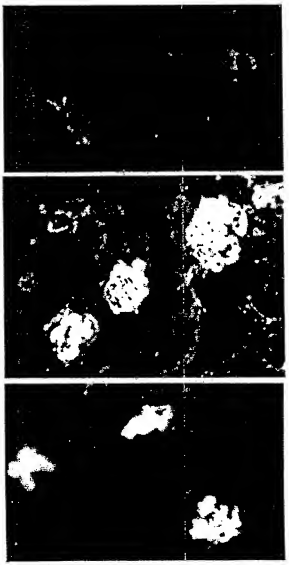

FIG. 2A

FIG. 2B

FIG. 2C

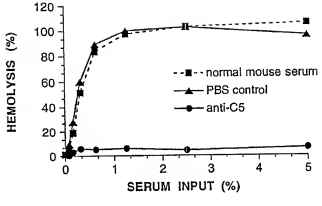
120
100
80
60
40
20
0
HEMOLYSIS (%)
0
1
2
3
4
5
SERUM INPUT (%)
normal mouse serum
PBS control
anti-C5

FIG. 3

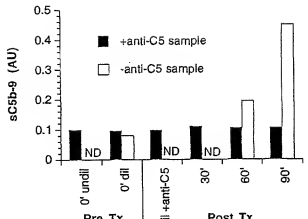
0.5
0.4
0.3
0.2
0.1
0
sC5b-9 (AU)
+anti-C5 sample
-anti-C5 sample
ND
ND
ND
0' undil
0' dil
0' dil +anti-C5
30'
60'
90'
Pre Tx
Post Tx

FIG. 4

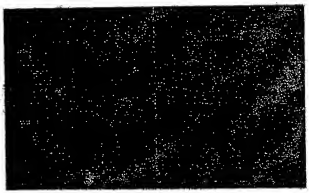

FIG. 5A

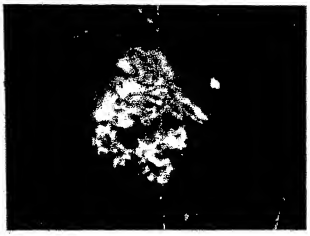

FIG.5B

FIG. 5C

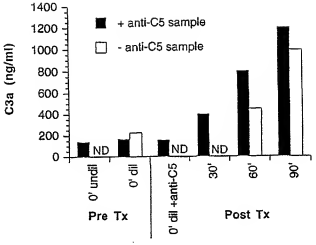
1400
1200
1000
800
600
400
200
0
C3a (ng/ml)
+ anti-C5 sample
- anti-C5 sample
ND
ND
ND
0' undil
0' dil
0' dil +anti-C5
30'
60'
90'
Pre Tx
Post Tx

FIG. 6

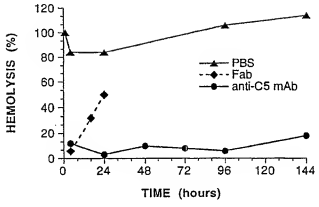
HEMOLYSIS (%)
120
100
80
60
40
20
0
0
24
48
72
96
120
144
TIME (hours)
PBS
Fab
anti-C5 mAb

FIG. 7A

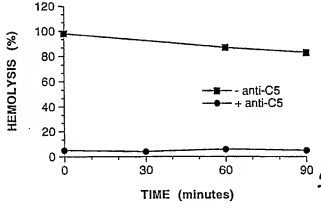
HEMOLYSIS (%)
120
100
80
60
40
20
0
0
30
60
90
TIME (minutes)
- anti-C5
+ anti-C5

FIG. 7B

2189015

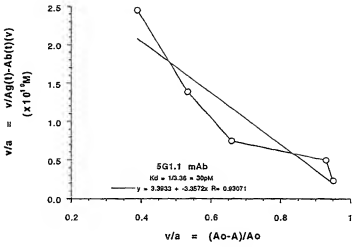

Fig. 8

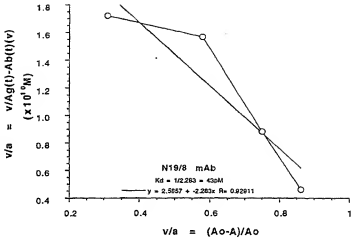
v/a = v/Ag(t)-Ab(t)(v)
(x10⁻⁹M)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.4
0.6
0.8
1
N19/8 mAb
Kd = 1/2.283 = 438M
y = 2.5557 + -2.283x R= 0.92911
v/a = (Ao-A)/Ao

Fig. 9

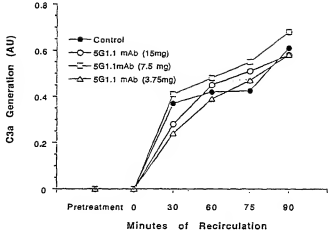
0.8
0.6
0.4
0.2
0
C3a Generation (AU)
Control
5G1.1 mAb (15mg)
5G1.1mAb (7.5 mg)
5G1.1 mAb (3.75mg)
Pretreatment 0 30 60 75 90
Minutes of Recirculation

Fig. 10

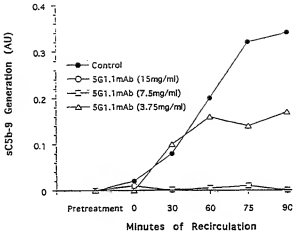
0.4
0.3
0.2
0.1
0
sC5b-9 Generation (AU)
Control
5G1.1mAb (15mg/ml)
5G1.1mAb (7.5mg/ml)
5G1.1mAb (3.75mg/ml)
Pretreatment 0 30 60 75 90
Minutes of Recirculation

Fig. 11

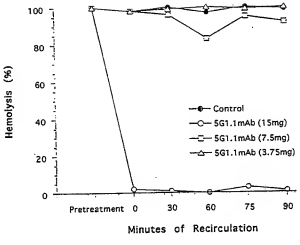
100
80
60
40
20
0
Hemolysis (%)
Control
5G1.1mAb (15mg)
5G1.1mAb (7.5mg)
5G1.1mAb (3.75mg)
Pretreatment 0 30 60 75 90
Minutes of Recirculation

Fig. 12

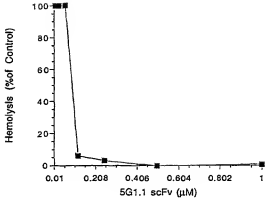
Hemolysis (%of Control)
100
80
60
40
20
0
0.01
0.208
0.406
0.604
0.802
1
5G1.1 scFv (µM)

Fig. 13

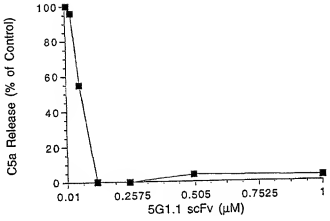
C5a Release (% of Control)
100
80
60
40
20
0
0.01
0.2575
0.505
0.7525
1
5G1.1 scFv (μM)

Fig. 14

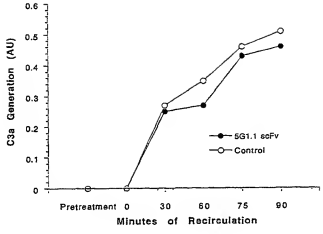
C3a Generation (AU)
0.6
0.5
0.4
0.3
0.2
0.1
0
5G1.1 scFv
Control
Pretreatment 0 30 60 75 90
Minutes of Recirculation

Fig. 15

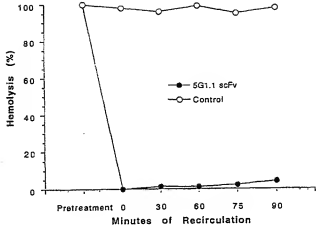
100
80
60
40
20
0
Hemolysis (%)
5G1.1 scFv
Control
Pretreatment 0 30 60 75 90
Minutes of Recirculation

Fig. 16

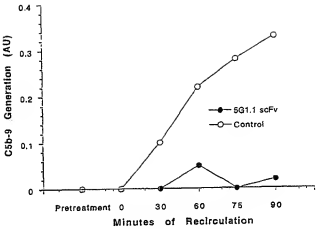
0.4
0.3
0.2
0.1
0
C5b-9 Generation (AU)
5G1.1 scFv
Control
Pretreatment 0 30 60 75 90
Minutes of Recirculation

Fig. 17

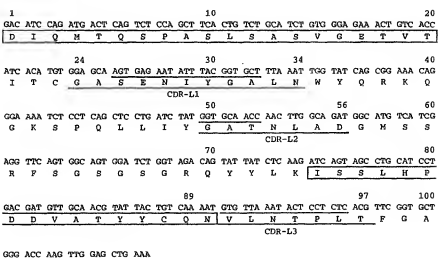
1 10 20
GAC ATC CAG ATG ACT CAG TCT CCA GCT TCA CTG TCT GCA TCT GTG GGA GAA ACT GTC ACC
D I Q M T Q S P A S L S A S V G E T V T
24 30 34 40
ATC ACA TGT GGA GCA AGT GAG AAT ATT TAC GGT GCT TTA AAT TGG TAT CAG CGG AAA CAG
I T C G A S E N I Y G A L N W Y Q R K Q
CDR-L1
50 56 60
GGA AAA TCT CCT CAG CTC CTG ATC TAT GGT GCA ACC AAC TTG GCA GAT GGC ATG TCA TCG
G K S P Q L L I Y G A T N L A D G M S S
CDR-L2
70 80
AGG TTC AGT GGC AGT GGA TCT GGT AGA CAG TAT TAT CTC AAG ATC AGT AGC CTG CAT CCT
R F S G S G S G R Q Y Y L K I S S L H P
89 97 100
GAC GAT GTT GCA ACG TAT TAC TGT CAA AAT GTG TTA AAT ACT CCT CTC ACG TTC GGT GCT
D D V A T Y Y C Q N V L N T P L T F G A
CDR-L3
GGG ACC AAG TTG GAG CTG AAA
G T K L E L K

Fig. 18

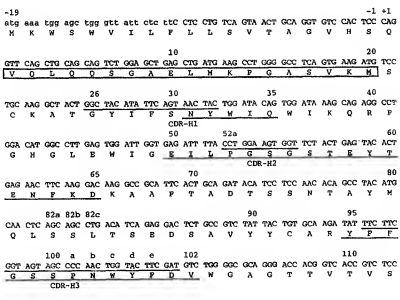
-19 -1 +1
atg aaa tgg agc tgg gtt att ctc ttc CTC CTG TCA GTA ACT GCA GGT GTC CAC TCC CAG
M K W S W V I L F L L S V T A G V H S Q
10 20
GTT CAG CTG CAG CAG TCT GGA GCT GAG CTG ATG AAG CCT GGG GCC TCA GTG AAG ATG TCC
V Q L Q Q S G A E L M K P G A S V K M S
26 30 35 40
TGC AAG GCT ACT GGC TAC ATA TTC AGT AAC TAC TGG ATA CAG TGG ATA AAG CAG AGG CCT
C K A T G Y I F S N Y W I Q W I K Q R P
CDR-H1
50 52a 60
GGA CAT GGC CTT GAG TGG ATT GGT GAG ATT TTA CCT GGA AGT GGT TCT ACT GAG TAC ACT
G H G L E W I G E I L P G S G S T E Y T
CDR-H2
65 70 80
GAG AAC TTC AAG GAC AAG GCC GCA TTC ACT GCA GAT ACA TCC TCC AAC ACA GCC TAC ATG
E N F K D K A A F T A D T S S N T A Y M
82a 82b 82c 90 95
CAA CTC AGC AGC CTG ACA TCA GAG GAC TCT GCC GTC TAT TAC TGT GCA AGA TAT TTC TTC
Q L S S L T S E D S A V Y Y C A R Y F F
100 a b c d e 102 110
GGT AGT AGC CCC AAC TGG TAC TTC GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC
G S S P N W Y F D V W G A G T T V T V S
CDR-H3
TCA
S

Fig. 19